

1 ttgcaggctg ctgggctggg gctaagggt gctcagtttc cttcagcggg gcaactgggaa  
 61 gcgccatggc actgcagggc atctcggtcg tggagctgtc cggcctggcc ccgggcccgt  
 121 tctgtgctat ggtcctggct gacttcgggg cgcgtgtggt acgcgtggac cggcccggct  
 181 cccgctacga cgtgagccgc ttgggcccgg gcaagcgctc gctagtgtg gacctgaagc  
 241 agccgcgggg agccgccgtg ctgcggcgtc tgtgcaagcg gtcggatgtg ctgctggagc  
 301 ccttcgcccg cgggtgtcatg gagaaactcc agctgggccc agagattctg cagcgggaaa  
 361 atccaaggct tatttatgcc aggetgagtg gatttgcca gtcaggaagc ttctgccggg  
 421 tagctggcca cgatatcaac tatttggtt tgtcaggtgt tctctcaaaa attggcagaa  
 481 gtggtgagaa tccgtatgcc ccgctgaatc tcttggtga ctttgctggg ggtggcctta  
 541 tgtgtgact gggcattata atggctcttt ttgaccgcac acgcactggc aagggtcagg  
 601 tcattgatgc aaatatggtg gaaggaacag catatttaag ttcttttctg tggaaaactc  
 661 agaaatcgag tctgtgggaa gcacctcgag gacagaacat gttggatggg ggagcacctt  
 721 tctatacgac ttacaggaca gcagatgggg aattcatggc tgttgagca atagaacccc  
 781 agttctacga gctgctgatc aaaggacttg gactaaagtc tgatgaactt cccaatcaga  
 841 tgagcatgga tgattggcca gaaatgaaga agaagtttgc agatgtattt gcaaagaaga  
 901 cgaaggcaga gtggtgtcaa atctttgacg gcacagatgc ctgtgtgact ccggttctga  
 961 cttttgagga ggttggtcat catgatcaca acaaggaacg gggctcgttt atcaccagt  
 1021 aggagcagga cgtgagcccc cgccctgcac ctctgctgtt aaacacccca gccatccctt  
 1081 ctttcaaaag ggatcctttc ataggagaac aactgagga gatacttgaa gaatttggat  
 1141 tcagccgcga agagatttat cagcttaact cagataaaat cattgaaagt aataaggtaa  
 1201 aagctagtct ctaacttcca ggcccacggc tcaagtgaat ttgaatactg catttacagt  
 1261 gtagagtaac acataacatt gtatgcatgg aaacatggag gaacagtatt acagtgtcct  
 1321 accactctaa tcaagaaaag aattacagac tctgattcta cagtgatgat tgaattctaa  
 1381 aaatggttat cattagggct tttgatttat aaaactttgg gtacttatac taaattatgg  
 1441 tagttattct gccttccagt ttgcttgata tatttggtga tattaagatt cttgacttat  
 1501 attttgaatg gggttctagtg aaaaaggaat gatataattc tgaagacatc gatatacatt  
 1561 tatttacact cttgattcta caatgtagaa aatgaggaaa tgccacaaat tgtatgggtga  
 1621 taaaagtcac gtgaaacaga gtgattgggt gcattccaggc cttttgtctt ggtgttcatg  
 1681 atctccctct aagcacattc caaactttag caacagttat cacactttgt aatttgcaaa  
 1741 gaaaagtttc acctgtattg aatcagaatg ccttcaactg aaaaaaacat atccaaaata  
 1801 atgaggaaat gtgttggtc actacgtaga gtccagaggg acagtcagtt ttaggggtgc  
 1861 ctgtatccag taactcgggg cctgtttccc cgtgggtctc tgggctgtca gctttccttt  
 1921 ctccatgtgt ttgatttctc ctcaggctgg tagcaagttc tggatcttat acccaacaca  
 1981 cagcaacatc cagaaataaa gttct

FIGURE 1

MALQGISVVELSGLAPGPF CAMVLADFGARVVRVDRPGSRYDVSRLGRGKRSLVLDLKQPRGA AVLRR LCK  
RSDV LLEPFRRGVMEKLQLGPEILQRENPR LIYARLSGFGQSGSFCRLAGHDINYLALSGVLSKIGRSGEN  
PYAPLNLLADFAGGGLMCALGIIMALFDRTGTGKGQVIDANMVEGTAYLSSFLWKTQKSSLWEAPRGQNML  
DGGAPFYTTYRTADGEFMAVGAI EPQFYELLIKGLGLKSDEL PNQMSMDDWPEMKKKFADVFAKKTAEWC  
QIFDGTDACVTPVLT FEEVVHHDHNKERGSFITSEEQDVSPRPAPLLLNTPAIP SFKRDPFIGEHTEEILE  
EFGFSREEIYQLNSDKIIESNKVKASL

09967303.097301

FIGURE 2

FIG. 3

SV1 (AMACR Isoform 1; >FMhxm\_44226FL01)  
 GGGCGCCGGGATTGGGAGGGCTTCTTGCAAGGCTGCTGGGCTGGGGCTAAG  
 GGCTGCTCAGTTTCCTTCAGCGGGGCACTGGGAAGCGCCATGGCACTGCA  
 GGGCATCTCGGTCTGTGGAGCTGTCCGGCCTGGCCCCGGGCGTCTGTG  
 CTATGGTCCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCC  
 GGCTCCCGCTACGACGTGAGCCGCTTGGGCGGGGCAAGCGCTCGCTAGT  
 GCTGGACCTGAAGCAGCCGCGGGGAGCCGCGTGTGCGGCGTCTGTGCA  
 AGCGGTCTGGATGTGCTGCTGGAGCCCTTCCGCCGCGGTGTCATGGAGAAA  
 CTCCAGCTGGGCCCAGAGATTCTGCAGCGGAAAATCCAAGGCTTATTTA  
 TGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTG  
 GCCACGATATCAACTATTTGGCTTTGTGTCAGGTGTTCTCTCAAAAATTGGC  
 AGAAGTGGTGAGAATCCGTATGCCCCGCTGAATCTCCTGGCTGACTTTGC  
 TGGTGGTGGCCTTATGTGTGCACTGGGCATTATAATGGCTCTTTTTTGACC  
 GCACACGCACTGGCAAGGGTCAGGTCAATTGATGCAAATATGGTGGAAAGGA  
 ACAGCATATTTAAGTTCTTTTCTGTGGAAACTCAGAAATCGAGTCTGTG  
 GGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTATA  
 CGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAA  
 CCCAGTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGA  
 ACTTCCCAATCAGATGAGCATGGATGATTGGCCAGAAATGAAGAAGAAGT  
 TTGCAGATGTATTTGCAAAGAAGACGAAGGCAGAGTGGTGTCAAATCTTT  
 GACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTTGAGGAGGTTGT  
 TCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAGC  
 AGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCAGCCATC  
 CCTTCTTTCAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACT  
 TGAAGAATTTGGATTCAGCCGCGAAGAGATTTATCAGCTTAACTCAGATA  
 AAATCATTGAAAGTAATAAGGTAAAAGCTAGTCTCTAACTTCCAGGCCCA  
 CGGCTCAAGTGAATTTGAATACTGCATTTACAGTGTAGAGTAACACATAA  
 CATTGTATGCATGGAAACATGGAGGAACAGTATTACAGTGTCTTACCACT  
 CTAATCAAGAAAAGAATTACAGACTCTGATTCTACAGTGATGATTGAATT  
 CTAAAAATGGTTATCATTAGGGCTTTTGATTTATAAACTTTGGGTACTT  
 AATACTAAATTATGGTAGTTATTCTGCCTTCCAGTTTGCTTGATATATTG  
 TTGATATTAAGATTCTTGACTTATATTTTGAATGGGTTCTAGTGAAAAAG  
 GAATGATATATTCTTGAAGACATCGATATACATTTATTTACACTCTTGAT  
 TCTACAATGTAGAAAATGAGGAAATGCCACAAATTGTATGGTGATAAAAG  
 TCACGTGAAACAGAGTGATTGGTTGCATCCAGGCCTTTTGTCTTGGTGTT  
 CATGATCTCCCTCTAAGCACATTCCAACTTTAGCAACAGTTATCACACT  
 TTGTAATTTGCAAAGAAAAGTTTCACCTGTATTGAATCAGAATGCCTTCA  
 ACTGAAAAAACATATCCAAAATAATGAGGAAATGTGTTGGCTCACTACG  
 TAGAGTCCAGAGGGACAGTCAGTTTTAGGGTTGCCTGTATCCAGTAACTC  
 GGGGCCTGTTTCCCCGTGGGTCTCTGGGCTGTGAGCTTTCCTTTCTCCAT  
 GTGTTTGATTTCTCCTCAGGCTGGTAGCAAGTTCTGGATCTTATACCCAA  
 CACACAGCAACATCCAGAAATAAAGATCTCAGGACCCCCCAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAA (SEQ ID NO:4)

FIG. 4

SV1 (>FMhxm\_44226FL01\_P1)  
MALQGISVVELSGLAPGPFCA\_MVLADFGARVVRVDRPGSRVDVSR\_LGRGKRSLVLDLKQP  
RGA\_AVLRLCKRSDVLLPEFRRGVM\_EKLQLGP\_EILQREN\_PRLIYARLSGFGQSGSF\_CRLA  
GHDINYLALSGVLSKIGRSGENPYAPLNLLAD\_FAGGGLM\_CALGIIMALFDRTRTGKGQVI  
DANMVEGTAYLSSFLWKTQKSSLWEAPRGQNMLDGGAPFYTTYRTADGEFMAVGAI\_EPQF  
YELLIKGLGLKSDEL\_PNQMSMDDWPEM\_KKKFADVFAKKT\_KAEWCQIFDGTDACVTPVLTF  
EEVVHHDH\_NKERGSFITSEEQDVSPRAP\_LLLNTPAIPSF\_KRDPFIGEHTTEEILEEFGFS  
REEIYQLNSDKIIESNKVKASL (SEQ ID NO:5)

SECRET

[illegible]

GGGCGCCGGGATTGGGAGGGCTTCTTGACAGGCTGCTGGGCTGGGGCTAAG  
GGCTGCTCAGTTTCCTTCAGCGGGGCACTGGGAAGCGCCATGGCACTGCA  
GGGCATCTCGGTCTGTGGAGCTGTCCGGCCTGGCCCCGGGCCCCGTTCTGTG  
CTATGGTCCTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGGCCC  
GGCTCCCGCTACGACGTGAGCCGCTTGGGCGGGGGCAAGCGCTCGCTAGT  
GCTGGACCTGAAGCAGCCGCGGGGAGCCGCCGTGCTGCGGCGTCTGTGCA  
AGCGGTTCGGATGTGCTGCTGGAGCCCTTCCGCCGCGGTGTCATGGAGAAA  
CTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAAAATCCAAGGCTTATTTA  
TGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTG  
GCCACGATATCAACTATTTGGCTTTGTTCAGGTGTTCTCTCAAAAATTGGC  
AGAAGTGGTGAGAATCCGTATGCCCCGCTGAATCTCCTGGCTGACTTTGC  
TGGTGGTGGCCTTATGTGTGCACTGGGCATTATAATGGCTCTTTTTTGACC  
GCACACGCACTGGCAAGGGTCAGGTCAATTGATGCAAATATGGTGGAAAGGA  
ACAGCATATTTAAGTTCTTTTCTGTGGAAACTCAGAAATCGAGTCTGTG  
GGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTATA  
CGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAA  
CCCCAGTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGA  
ACTTCCCAATCAGATGAGCATGGATGATTGGCCAGAAATGAAGAAGAAGT  
TTGCAGATGTATTTGCAAAGAAGACGAAGGCAGAGTGGTGTCAAATCTTT  
GACGGCACAGATGCCTGTGTGACTCCGGTTCTGACTTTTGAGGAGGTTGT  
TCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAGC  
AGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTAAACACCCAGCCATC  
CCTTCTTTCAAAAGGGATCCTTTTCATAGGAGAACACACTGAGGAGATACT  
TGAAGAATTTGGATTCAGCCGCGAAGAGATTTATCAGCTTAACTCAGATA  
AAATCATTGAAAGTAATAAGGCTGGTAGCAAGTTCTGGATCTTATACCCA  
ACACACAGCAACATCCAGAAATAAAGATCTCAGGACCCCCCAGCAAGTCG  
TTTTGTGTCTCCTTGGACTGAGTTAAGTTACAAGCCTTTCTTATACCTGT  
CTTTGACAAAGAAGACGGGATTGTCTTTACATAAAACCAGCCTGCTCCTG  
GAGCTTCCCTGGACTCAACTTCCTAAAGGCATGTGAGGAAGGGGTAGATT  
CCACAATCTAATCCGGGTGCCATCAGAGTAGAGGGAGTAGAGAATGGATG  
TTGGGTAGGCCATCAATAAGGTCCATTCTGCGCAGTATCTCAACTGCCGT  
TCAACAATCGCAAGAGGAAGGTGGAGCAGGTTTCTTCATCTTACAGTTGA  
GAAAACAGAGACTCAGAAGGGCTTCTTAGTTTCATGTTTCCCTTAGCGCCT  
CAGTGATTTTTTTCATGGTGGCTTAGGCCAAAAGAAATATCTAACCATTCA  
ATTTATAAATAATTAGGTCCCCAACGAATTAAATATTATGTCCTACCAAC  
TTATTAGCTGCTTGAAAAATATAATACACATAAAATAAAAAAATATATTTT  
TCATTTCTATTTTATTGTTAATCACAACACTACTACTAAGGAGATGTATGC  
ACCTATTGGACACTGTGCAACTTCTCACCTGGAATGAGATTGGACACTGC  
TGCCCTCATTTTCTGCTCCATGTTGGTGTCCATATAGTACTTGATTTTTT  
ATCAGATGGCCTGGAAAACCCAGTCTCACAAAAATATGAAATTATCAGAA  
GGATTATAGTGCAATCTTATGTTGAAAGAATGAACTACCTCACTAGTAGT  
TCACGTGATGTCTGACAGATGTTGAGTTTCATTGTGTTTGTGTGTTCAAA  
TTTTTAAATATTCTGAGATACTCTTGTGAGGTCACTCTAATGCCCTGGGT  
GCCTTGGCACAGTTTTTAGAAATACCAGTTGAAAATATTTGCTCAGGAATA  
TGCAACTAGGAAGGGGCAGAATCAGAAATTAAGCTTTCATATTCTAGCCT  
TCAGTCTTGTTCTTCAACCATTTTTTAGGAACTTTCCCATAGGTTATGTT  
TTCCAGCCCAGGCATGGAGGATCACTTGAGGCCAAGAGTTCGAGACCAGC  
CTGGGGAACTTGGCTGGACCTCCGTTTCTACGAAATAAAAAATAAAAAAAT  
TATCCAGGTATGGTGGTGTGTGCCTGTAGTCCTATCTACTCAAGGGTGGG

FIG. 5B

GCAGGAGGATCACTTGAGCCCAGGAATTTGAGGCCACAGTGAATTAGGAT  
TGCACCACTGCACTCTAGCCCAGGCAACAGAACAAGAACCTGTCTCTAAA  
TAAATAAATAAAAAATAATAATAAAAAAGATGTTTTCCCTACAAAAA  
GACTTTTCATTTGAACTCGGTCCAGCAAGGAAAATATAACCCACTCGAAG  
TCTTTAAACAGAGGAAATTTAATATAAAGAATTCCACTGGTGACGAAAG  
AGCAGAGAAGCCCAGAAGATAGTGAGGCAACCCTGATAGGAACATAACTA  
GGAAGCCAAGACCACTCCTATGGTTGCAGGGGTGATGGGAAAGCTGGTGT  
ACTTGGACCCAGAAGCCAAAGTTGCTGCACCCACCTTGGAGACATAGACA  
CTGGCAGTAATACCTCAGGGAGAAGAAAGAAATCTAGGGAAATATCCTGG  
CTTCTTTCCTTCTCTCTCTCCCTAGTCTTCCTACCAGTGTCTCCCATTA  
GCCAAATCTACCTAGAAGCCAGAAAACAAGGGAACCCTGGAAATGTAGCC  
CCATAAGATAAAGAGCACCAAAGGAAATAGATCTGAGCAGACAGGCAGCA  
CAAAATGCAGTGTGTATGGTTTATTCCTCAGTAATTCCTTTAGCAAATG  
TTTATTGAGGATCTACTAGGTGCCAGGTATCATGATACTTGCTGGGGATA  
CCATAATGAACAAAACAGACCTGTTCTCCGCTCTTGAGGAAATCAAAGAC  
AAACACAGGATATGGAATAAACCAGAATTATCTCATTGTAAAATGTGTT  
AAGTACCACGAGGAGAAATATCAGGGCCATCTGACACAGCTAATGATTG  
AAGAAGGGTGTGACCTGCCACCATTTTAAATCTAGTTATTTCACTCCTGA  
GCTGTGTGTGTGGAAAACCTGTAGTAAAAAATAGAATGTCTATATTTATA  
AAAAGTTTATGAAAAGATATCAATTTATTTACATTTTGACAAACTCTATG  
TAATAAGGCTTTATTACTCACGGCCATGTGTGTGATCATGTGTAATAGCA  
TGTGTGTATGAGAGAGAGAAGCCATATGTAATTATGTGTAATAACGTCTG  
TGAGAGAGAAGCCATGTGTGTGATCATGTAAAATAACGTGTGTGAGAGAA  
GCCATGTGTGTGATCGTGTAAAATAACGTGTGTGAGAAGCCGTGTGTGAT  
GTGT (SEQ ID NO:6)

096705-09201

FIG. 6

SV2 (>FMhXm\_44226FL02\_P1)

MALQGISVVELSGLAPGPF CAMVLADFGARVVRVDRPGSRYDVSRLGRGKRSLVLDLKQP  
RGA AVLRR LCKRSDV LLEPFRRGVMEKLQLGPEILQRENPR LIYARLSGFGQSGSFCRLA  
GHDINYLALSGVLSKIGRSGENPYAPLNLLADFAGGGLMCALGIIMALFDRTRTDKGQVI  
DANMVEGTAYLSSFLWKTQKSSLWEAPRGQNMLDGGAPFYTTYRTADGEFMAVGAIEPQF  
YELLIKGLGLKSDELPNQMSMDDWPEMKKKFADVFAKKTAEWCQIFDGTDACVTPVLT  
EEVVHHDHNKERGSFITSEEQDVSPRPAPLLLNTPAIPSFKRDPFIGEHTEEILEEFGFS  
REEIYQLNSDKIIESNKAGSKFWILYPHTHSNIQK (SEQ ID NO:7)

0957305-092804  
100260-507950

[illegible]

GGGCGCCGGGATTGGGAGGGCTTCTTGCAGGCTGCTGGGCTGGGGCTAAG  
GGCTGCTCAGTTTCTTTCAGCGGGGCACTGGGAAGCGCCATGGCACTGCA  
GGGCATCTCGGTCTGTGGAGCTGTCCGGCCTGGCCCCGGGCCCCGTTCTGTG  
CTATGGTCTTGGCTGACTTCGGGGCGCGTGTGGTACGCGTGGACCGGCCC  
GGCTCCCGCTACGACGTGAGCCGCTTGGGCCCCGGGCAAGCGCTCGCTAGT  
GCTGGACCTGAAGCAGCCGCGGGGAGCCGCCGTGCTGCGGCGTCTGTGCA  
AGCGGTCTGGATGTGCTGCTGGAGCCCTTCCGCCGCGGTGTCATGGAGAAA  
CTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAAAAATCCAAGGCTTATTTA  
TGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTAGCTG  
GCCACGATATCAACTATTTGGCTTTGTGAGGTGGAAGGAACAGCATATTT  
AAGTTCTTTTTCTGTGGAAAACTCAGAAATCGAGTCTGTGGGAAGCACCTC  
GAGGACAGAACATGTTGGATGGTGGAGCACCTTTCTATACGACTTACAGG  
ACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCAAGTTCTA  
CGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATC  
AGATGAGCATGGATGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGTA  
TTTGCAAAGAAGACGAAGGCAGAGTGGTGTCAAATCTTTGACGGCACAGA  
TGCCTGTGTGACTCCGGTTCTGACTTTTGAGGAGGTTGTTTCATCATGATC  
ACAACAAGGAACGGGGCTCGTTTATCACCAGTGAGGAGCAGGACGTGAGC  
CCCCGCCCTGCACCTCTGCTGTAAACACCCCAGCCATCCCTTCTTTCAA  
AAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTG  
GATTCAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAA  
AGTAATAAGGTAAAAGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTG  
AATTTGAATACTGCATTTACAGTGTAGAGTAACACATAACATTGTATGCA  
TGGAACATGGAGGAACAGTATTACAGTGTCTTACCCTCTAATCAAGAA  
AAGAATTACAGACTCTGATTCTACAGTGATGATTGAATTCTAAAAATGGT  
TATCATTAGGGCTTTTTGATTTATAAACTTTGGGTACTTATACTAAATTA  
TGGTAGTTATTCTGCCTTCCAGTTTGCTTGATATATTTGTTGATATTAAG  
ATTCTTGACTTATATTTTGAATGGGTCTAGTGAAAAAGGAATGATATAT  
TCTTGAAGACATCGATATACATTTATTTACACTCTTGATTCTACAATGTA  
GAAAATGAGGAAATGCCACAAATTGTATGGTGATAAAAGTCACGTGAAAC  
AGAGTGATTGGTTGCATCCAGGCCTTTTGTCTTGGTGTTCATGATCTCCC  
TCTAAGCACATTCCAAACTTTAGCAACAGTTATCACACTTTGTAATTTGC  
AAAGAAAAGTTTCACCTGTATTGAATCAGAATGCCTTCAACTGAAAAAA  
CATATCCAAAATAATGAGGAAATGTGTTGGCTCACTACGTAGAGTCCAGA  
GGGACAGTCAGTTTTAGGGTTGCCTGTATCCAGTAACTCGGGGCCTGTTT  
CCCCGTGGGTCTCTGGGCTGTCAGCTTTCCTTTCTCCATGTGTTTGATTT  
CTCCTCAGGCTGGTAGCAAGTTCTGGATCTTATACCCAACACACAGCAAC  
ATCCAGAAATAAAGATCTCAGGACCCCCCAGCAAGTCGTTTTGTGTCTCC  
TTGGACTGAGTTAAGTTACAAGCCTTTCTTATACCTGTCTTTGACAAAGA  
AGACGGGATTGTCTTTACATAAAACCAGCCTGCTCCTGGAGCTTCCCTGG  
ACTCAACTTCCTAAAGGCATGTGAGGAAGGGGTAGATTCCACAATCTAAT  
CCGGGTGCCATCAGAGTAGAGGGAGTAGAGAATGGATGTTGGGTAGGCCA  
TCAATAAGGTCCATTCTGCGCAGTATCTCAACTGCCGTTCAACAATCGCA  
AGAGGAAGGTGGAGCAGGTTTCTTCATCTTACAGTTGAGAAAAACAGAGAC  
TCAGAAAGGGCTTCTTAGTTTCATGTTTCCCTTAGCGCCTCAGTGATTTTTT  
CATGGTGGCTTAGGCCAAAAGAAATATCTAACCATTCAATTTATAAATAA  
TTAGGTCCCCAACGAATTAAATATTATGTCCTACCAACTTATTAGCTGCT  
TGAAAAATATAATACACATAAAATAAAAAAATATATTTTTTCATTTCTATTT  
CATTGTTAATCACAACTACTTACTAAGGAGATGTATGCACCTATTGGACA



FIG. 7B

CTGTGCAACTTCTCACCTGGAATGAGATTGGACACTGCTGCCCTCATTTT  
CTGCTCCATGTTGGTGTCCATATAGTACTTGATTTTTTATCAGATGGCCT  
GGAAAACCCAGTCTCACAAAAATATGAAATTATCAGAAGGATTATAGTGC  
AATCTTATGTTGAAAGAATGAACTACCTCACTAGTAGTTCACGTGATGTC  
TGACAGATGTTGAGTTTCATTGTGTTTGTGTGTTCAAATTTTTTAAATATT  
CTGAGATACTCTTGTGAGGTCACCTCTAATGCCCTGGGTGCCTTGGCACAG  
TTTTAGAAATACCAGTTGAAAATATTTGCTCAGGAATATGCAACTAGGAA  
:GGGGCAGAATCAGAATTTAAGCTTTCATATTCTAGCCTTCAGTCTTGTT  
CTTCAACCATTTTTAGGAACTTTCCCATAGGTTATGTTTTCCAGCCCAG  
GCATGGAGGATCACTTGAGGCCAAGAGTTTCGAGACCAGCCTGGGGAACTT  
GGCTGGACCTCCGTTTCTACGAAATAAAAATAAAAAAATTATCCAGGAAA  
AAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:8)

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[illegible]

MALQGISVVELSGLAPGPF CAMVLADFGARVVRVDRPGSRYDVSRLGRGKRSLVLDLKQP  
RGA AVLRLCKRSDVLLPEFRRGVMEKLQLGPEILQRENPR LIYARLSGFGQSGSFCRLA  
GHDINY LALSGGRNSIFKFFSVENSEIESVGSTSRTEHVGWWSTFLYDLQDSRWGIHGCW  
SNRTPVLRAADQRTWTKV (SEQ ID NO:9)

FIG. 9

SV4 (AMACR Isoform 4; >gi|14725916|ref|XM\_043772.1| Homo sapiens alpha-methylacyl-CoA racemase (AMACR), mRNA)

TTGCAGGCTGCTGGGCTGGGGCTAAGGGCTGCTCAGTTTCCTTCAGCGGG  
GCACTGGGAAGCGCCATGGCACTGCAGGGCATCTCGGTCGTGGAGCTGTC  
CGGCCTGGCCCCGGGCCCCGTTCTGTGCTATGGTCCTGGCTGACTTCGGGG  
CGCGTGTGGTACGCGTGGACCGGCCCCGGCTCCCGCTACGACGTGAGCCGC  
TTGGGCCGGGGCAAGCGCTCGCTAGTGCTGGACCTGAAGCAGCCGCGGGG  
AGCCGCCGTGCTGCGGCGTCTGTGCAAGCGGTGCGATGTGCTGCTGGAGC  
CCTTCCGCCGCGGTGTCATGGAGAACTCCAGCTGGGCCCAGAGATTCTG  
CAGCGGGAATAATCCAAGGCTTATTTATGCCAGGCTGAGTGGATTGCGCA  
GTCAGGAAGCTTCTGCCGGTTAGCTGGCCACGATATCAACTATTTGGCTT  
TGTCAGGTGTTCTCTCAAAAATTGGCAGAAGTGGTGAGAATCCGTATGCC  
CCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTATGTGTGCACT  
GGGCATTATAATGGCTCTTTTTGACCGCACACGCACTGGCAAGGGTCAGG  
TCATTGATGCAAATATGGTGGAAGGAACAGCATATTTAAGTTCTTTTCTG  
TGGAATACTCAGAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACAT  
GTTGGATGGTGGAGCACCTTTCTATACGACTTACAGGACAGCAGATGGGG  
AATTCATGGCTGTTGGAGCAATAGAACCCAGTTCTACGAGCTGCTGATC  
AAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGATGAGCATGGA  
TGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTTGCAAAGAAGA  
CGAAGGCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACT  
CCGGTTCTGACTTTTGAGGAGGTTGTTTCATCATGATCACAACAAGGAACG  
GGGCTCGTTTATCACCAGTGAGGAGCAGGACGTGAGCCCCCGCCCTGCAC  
CTCTGCTGTTAAACACCCCAGCCATCCCTTCTTTCAAAGGGATCCTTTC  
ATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATTGAGCCGCGA  
AGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAA  
AAGCTAGTCTCTAACTTCCAGGCCACGGCTCAAGTGAATTTGAATACTG  
CATTTACAGTGTAGAGTAACACATAACATTGTATGCATGGAAACATGGAG  
GAACAGTATTACAGTGTCTTACCCTCTAATCAAGAAAAGAATTACAGAC  
TCTGATTCTACAGTGATGATTGAATTCTAAAAATGGTTATCATTAGGGCT  
TTTGATTTATAAACTTTGGGTACTTATACTAAATTATGGTAGTTATTCT  
GCCTTCCAGTTTGCTTGATATATTTGTTGATATTAAGATTCTTGACTTAT  
ATTTTGAATGGGTTCTAGTGAAAAAGGAATGATATATTCTTGAAGACATC  
GATATACATTTATTTACACTCTTGATTCTACAATGTAGAAAATGAGGAAA  
TGCCACAAATTGTATGGTGATAAAAGTCACGTGAAACAGAGTGATTGGTT  
GCATCCAGGCCTTTTGTCTTGGTGTTTCATGATCTCCCTCTAAGCACATTC  
CAAACTTTAGCAACAGTTATCACACTTTGTAATTTGCAAAGAAAAGTTTC  
ACCTGTATTGAATCAGAATGCCTTCAACTGAAAAAACATATCCAAAATA  
ATGAGGAAATGTGTTGGCTCACTACGTAGAGTCCAGAGGGACAGTCAGTT  
TTAGGGTTGCCTGTATCCAGTAACTCGGGGCCTGTTTCCCCGTGGGTCTC  
TGGGCTGTGAGCTTTCCTTTCTCCATGTGTTTGATTTCTCCTCAGGCTGG  
TAGCAAGTTCTGGATCTTATACCAACACACAGCAACATCCAGAAATAAA  
GATCT (SEQ ID NO:10)

0597305 "0597305"

Age group	Gender	Number of cases	Number of deaths	Number of survivors	Number of cases with complications	Number of cases with sequelae	Number of cases with long-term sequelae	Number of cases with death
0-14	Male	10	0	10	0	0	0	0
0-14	Female	10	0	10	0	0	0	0
15-24	Male	10	0	10	0	0	0	0
15-24	Female	10	0	10	0	0	0	0
25-34	Male	10	0	10	0	0	0	0
25-34	Female	10	0	10	0	0	0	0
35-44	Male	10	0	10	0	0	0	0
35-44	Female	10	0	10	0	0	0	0
45-54	Male	10	0	10	0	0	0	0
45-54	Female	10	0	10	0	0	0	0
55-64	Male	10	0	10	0	0	0	0
55-64	Female	10	0	10	0	0	0	0
65-74	Male	10	0	10	0	0	0	0
65-74	Female	10	0	10	0	0	0	0
75-84	Male	10	0	10	0	0	0	0
75-84	Female	10	0	10	0	0	0	0
85-94	Male	10	0	10	0	0	0	0
85-94	Female	10	0	10	0	0	0	0
95-104	Male	10	0	10	0	0	0	0
95-104	Female	10	0	10	0	0	0	0
105-114	Male	10	0	10	0	0	0	0
105-114	Female	10	0	10	0	0	0	0
115-124	Male	10	0	10	0	0	0	0
115-124	Female	10	0	10	0	0	0	0
125-134	Male	10	0	10	0	0	0	0
125-134	Female	10	0	10	0	0	0	0
135-144	Male	10	0	10	0	0	0	0
135-144	Female	10	0	10	0	0	0	0
145-154	Male	10	0	10	0	0	0	0
145-154	Female	10	0	10	0	0	0	0
155-164	Male	10	0	10	0	0	0	0
155-164	Female	10	0	10	0	0	0	0
165-174	Male	10	0	10	0	0	0	0
165-174	Female	10	0	10	0	0	0	0
175-184	Male	10	0	10	0	0	0	0
175-184	Female	10	0	10	0	0	0	0
185-194	Male	10	0	10	0	0	0	0
185-194	Female	10	0	10	0	0	0	0
195-204	Male	10	0	10	0	0	0	0
195-204	Female	10	0	10	0	0	0	0
205-214	Male	10	0	10	0	0	0	0
205-214	Female	10	0	10	0	0	0	0
215-224	Male	10	0	10	0	0	0	0
215-224	Female	10	0	10	0	0	0	0
225-234	Male	10	0	10	0	0	0	0
225-234	Female	10	0	10	0	0	0	0
235-244	Male	10	0	10	0	0	0	0
235-244	Female	10	0	10	0	0	0	0
245-254	Male	10	0	10	0	0	0	0
245-254	Female	10	0	10	0	0	0	0
255-264	Male	10	0	10	0	0	0	0
255-264	Female	10	0	10				

MALQGISVVELSGLAPGPF CAMVLADFGARVVRVDRPGSRYDVSRLGRGKRS LVLDLKQP  
RGA AVLRR LCKRSDV LLEPFRRGVMEKLQLGP EILQRENPR LIYARLSGFGQSGSFCRLA  
GHDINYLALSGVLSKIGRSGENPYAPL NLLADFAGGGLMCALGI IMA LFDRTTRTGKGQVI  
DANMVEGTAYLSSFLWKTQKSSLWEAPRGQNMLDGGAPFYTTYRTADGEFMAVGAIEPQF  
YELLIKGLGLKSDEL PNQMSMDDWPEMKKKFADVFAKKTAEWCQIFDGTDACVTPVLTF  
EEVVHHDHNKERGSFITSEEQDVSPRPAPLLLNTPAIP SFKRDPFIGEHTEEILEEFGFS  
REEIYQLNSDKIIESNKVKASL (SEQ ID NO:11)

TABLE 2 "30E/3660"

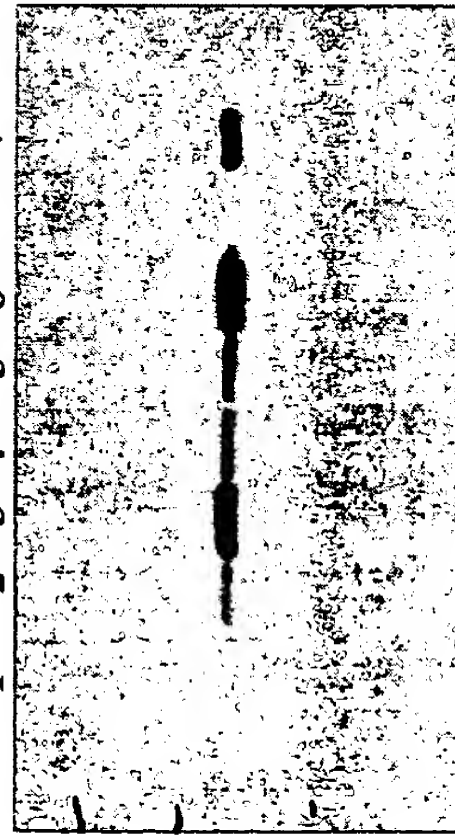
- |                            |                         |
|----------------------------|-------------------------|
| 1) normal prostate         | 7) normal colon         |
| 2) prostate adenocarcinoma | 8) colon adenocarcinoma |
| 3) prostate adenocarcinoma | 9) liver met (colon)    |
| 4) lymph node met (prost)  | 10) normal liver        |
| 5) liver met (prost)       | 11) normal kidney       |
| 6) liver met (prost)       | 12) normal kidney       |
|                            | 13) normal brain        |
|                            | 14) normal muscle       |
|                            | 15) normal muscle       |

1 2 3 4 5 6 + 7 8 9 10 11 12 13 14 15



ML 185

1 2 3 4 5 6 + 7 8 9 10 11 12 13 14 15

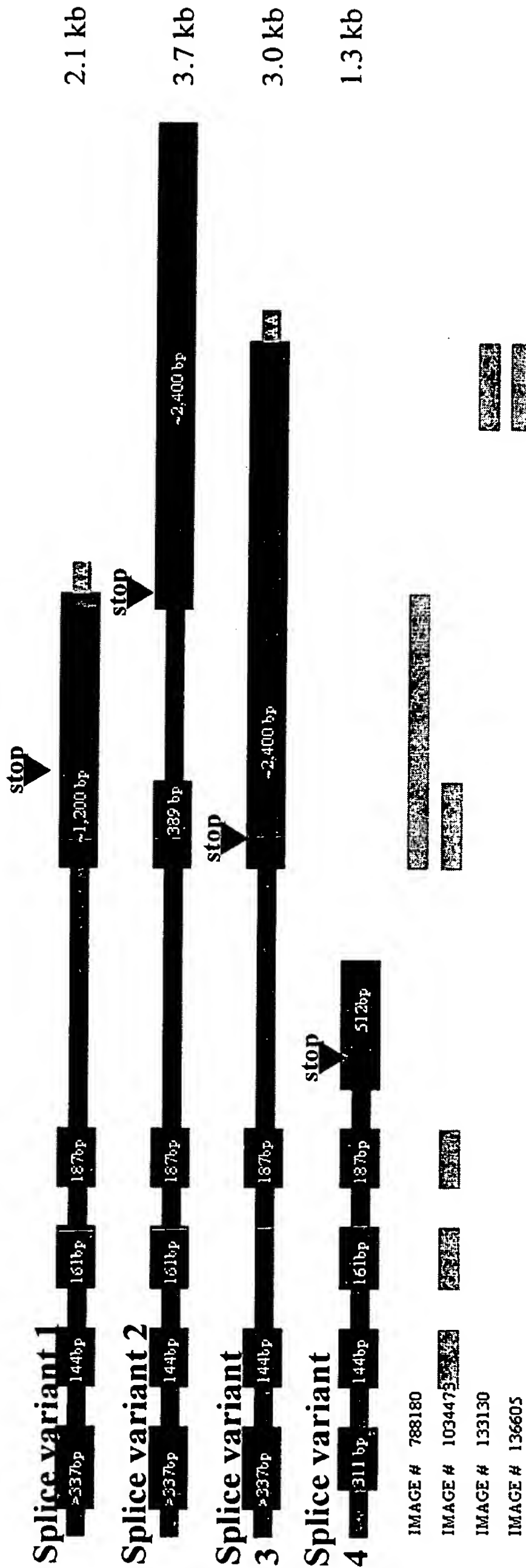


ML 186

FIG. 11

FIG. 12

# Racemace splice variants identified by sequencing of IMAGE clones





TOPSEED 60729650

IMAGE clone 136605

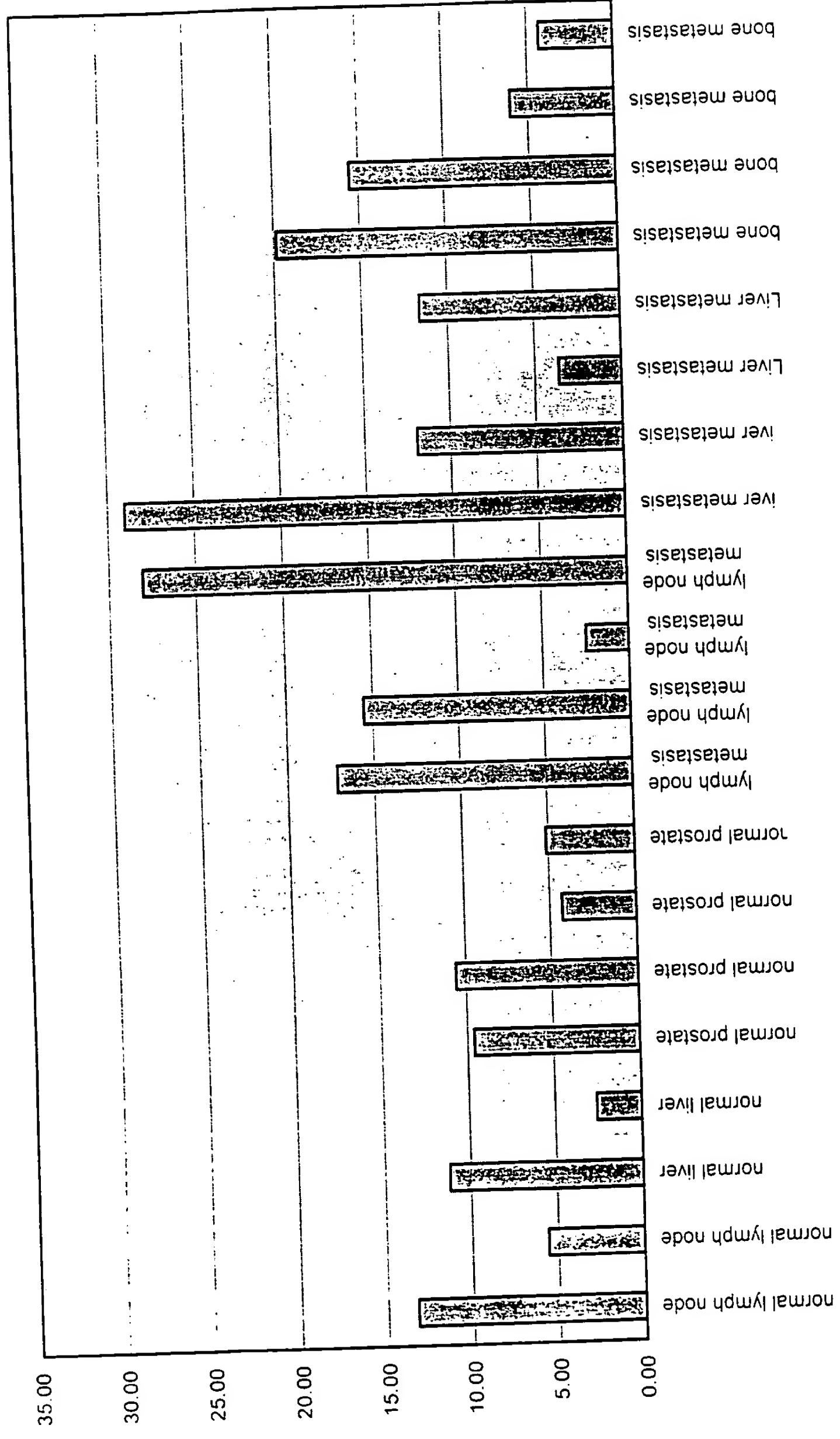


FIG. 14A



T03260" 9029560

IMAGE clone 133130

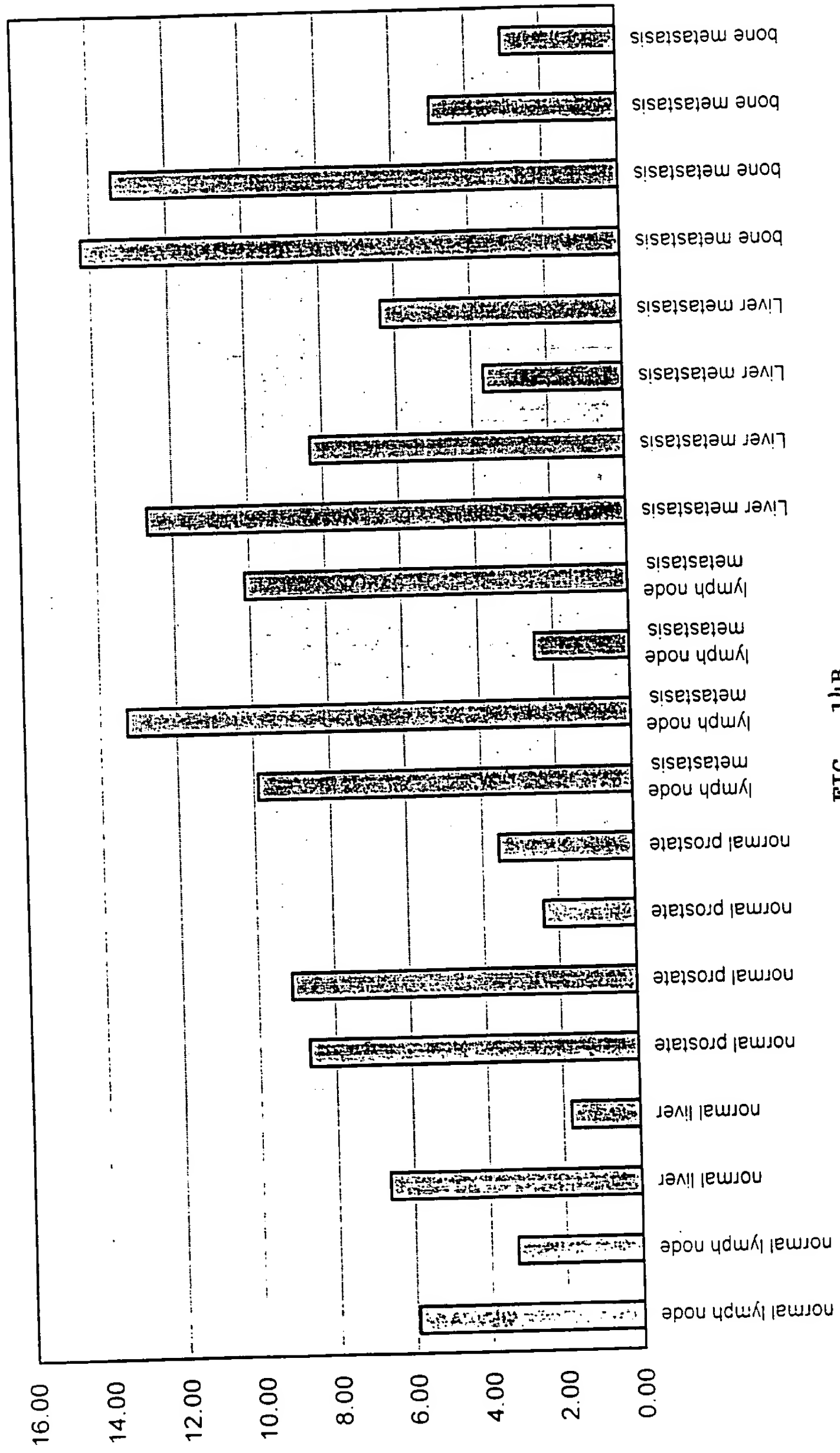


FIG. 14B

TOP SECRET 9660

IMAGE clone 1034473: MID=44226 alpha-methylacyl-CoA racemase

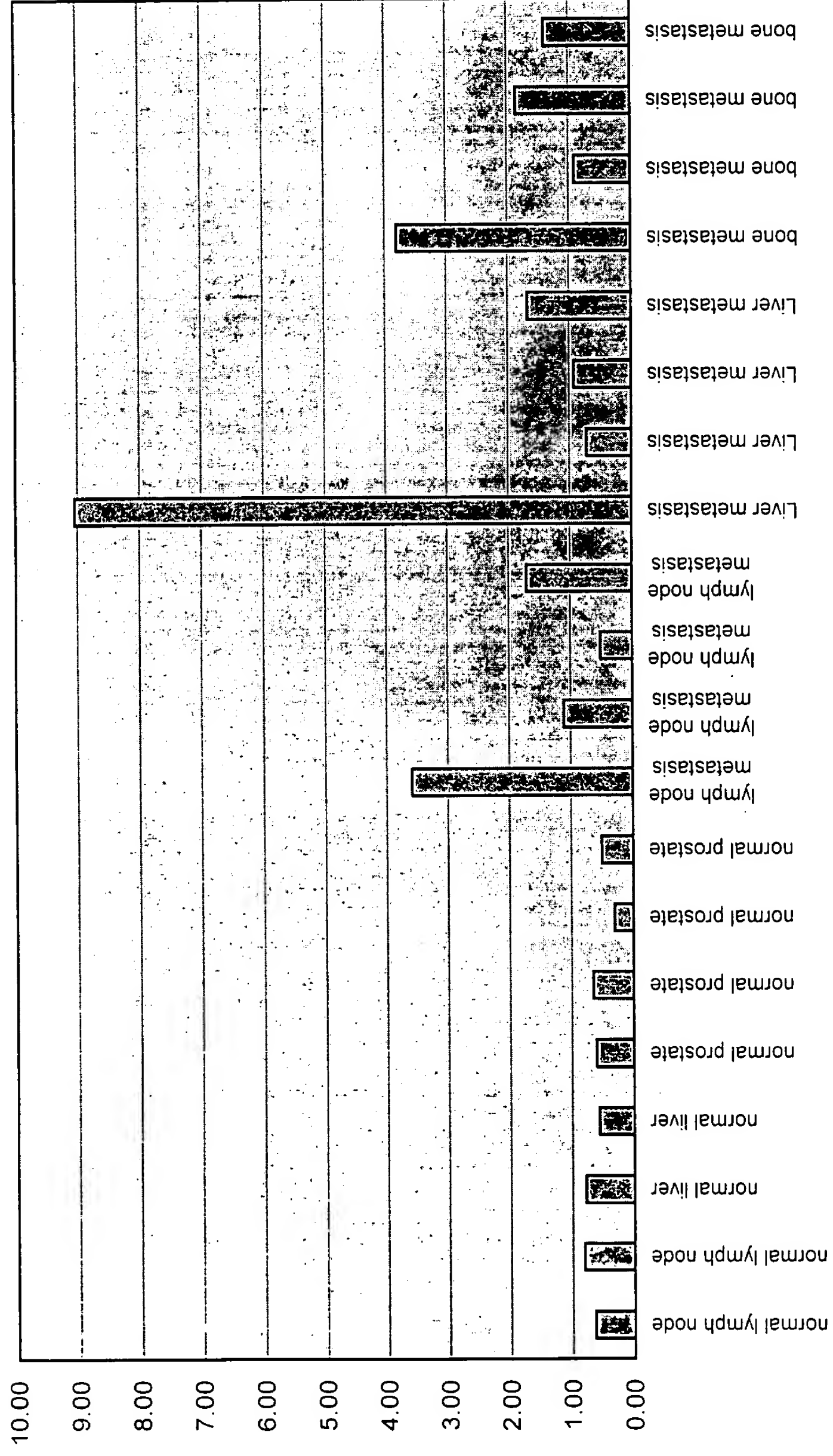


FIG. 14C

708260" 502960

IMAGE clone 788180: MID=44226 alpha-methylacyl-CoA racemase

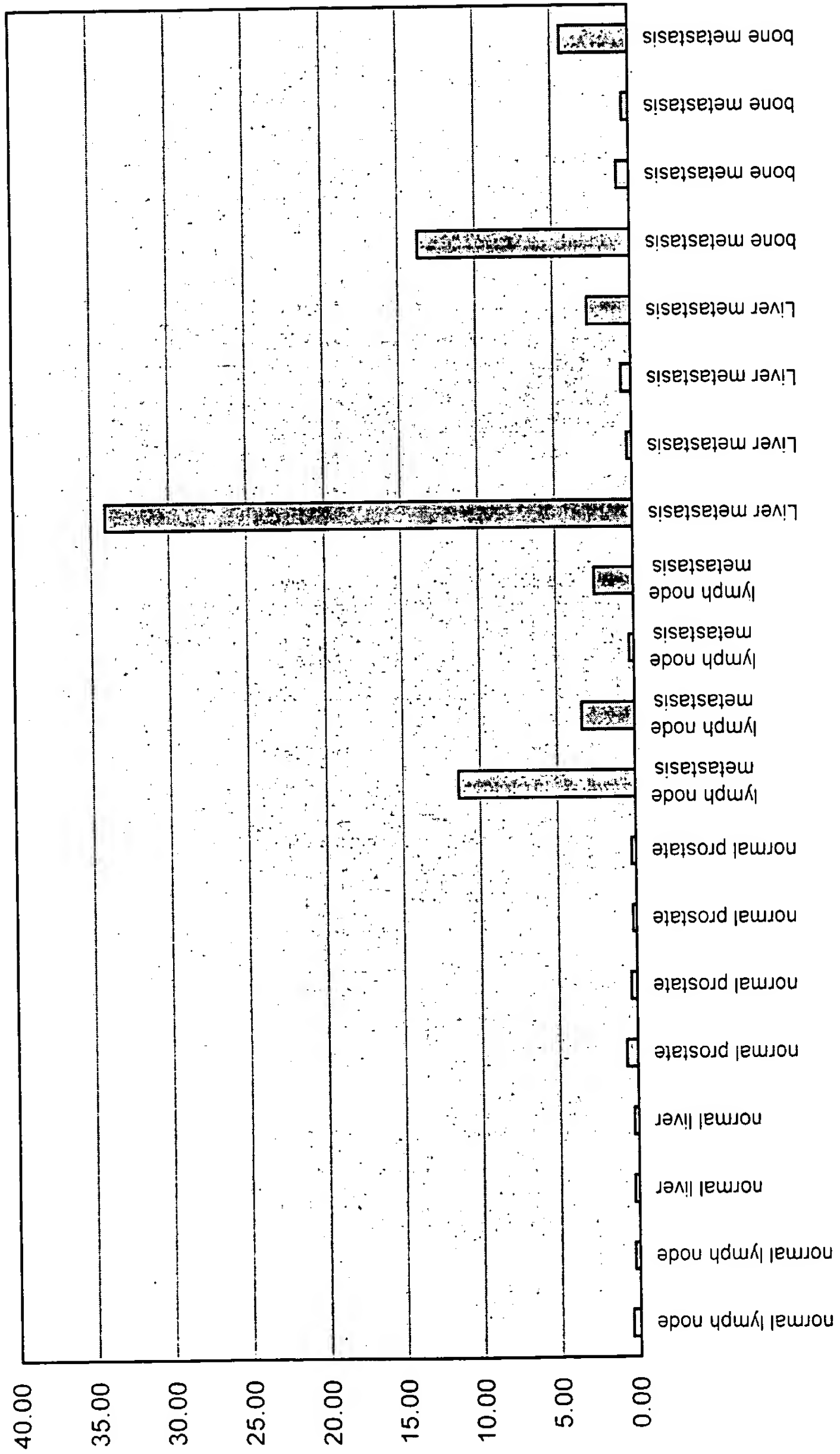


FIG. 14D